

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/902,705

DATE: 10/17/2001

TIME: 07:24:57

Input Set : N:\Crf3\10152001\I902705.raw

Output Set: N:\CRF3\10172001\I902705.raw

1 <110> APPLICANT: Bednarik et al.
2 <120> TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
3 <130> FILE REFERENCE: PF138P1C1
4 <140> CURRENT APPLICATION NUMBER: US/09/902,705
5 <141> CURRENT FILING DATE: 2001-07-12
6 <150> PRIOR APPLICATION NUMBER: US 08/461,031
7 <151> PRIOR FILING DATE: 1995-06-05
8 <150> PRIOR APPLICATION NUMBER: PCT/US94/11914
9 <151> PRIOR FILING DATE: 1994-10-19
10 <160> NUMBER OF SEQ ID NOS: 11
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1386
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (626)..(1264)
20 <223> OTHER INFORMATION:
21 <400> SEQUENCE: 1

22	gattttttgt gatatttct tccggggggg ggggaacctt ttgtataaac gccaaaccaac	60
23	cggccctttt ttgggtacct ggccatttta cttggcccat ttgggtaaaa tgttcctttc	120
24	cctgcgttaa tccccctgat tccttgtagg ataaccgcta tccccccct tagagtgaat	180
25	ttgaaaacct ttccgcccgg aaggggaccg accgagccca gcgattcatg gagcgaggaa	240
26	agcgggaaga gcgcccaata cccaagccgc ctctgcgcgg cgcgttggtgc gattcattaa	300
27	tacagctgcc acgacaggtt tcccgaactg aaagcgggta gtgagcgcaa cacaattaat	360
28	gtgagtttag tcaactatta ggcaccccag gcttttacct ttatgcttcc ggctcgtatg	420
29	ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac	480
30	gtccaagctc gaaattaacc ctcaactaaag ggaacaaaaa ctggagctcc accgcggtgg	540
31	cggccgctct agaactagt gatcccccg gctccaggaa ttccgccaga ccgggaggac	600
32	cgaggaggcg ccagactacg ggcga atg gcg acc cgc agc cct ggc gtc gtg	652
33		
34	Met Ala Thr Arg Ser Pro Gly Val Val	
35	1 5	
36	att atg gat gat tgg cca ggg tat gac ttg aat tta ttc acg tac cca	700
37	Ile Met Asp Asp Trp Pro Gly Tyr Asp Leu Asn Leu Phe Thr Tyr Pro	
38	10 15 20 25	
39	cag cac tat tat gga gac ttg gag tat gtc ctc atc cct cat ggt atc	748
40	Gln His Tyr Tyr Gly Asp Leu Glu Tyr Val Leu Ile Pro His Gly Ile	
41	30 35 40	
42	att gtg gac aga att gag cgg ctg gcc aag gat att atg aaa gac ata	796
43	Ile Val Asp Arg Ile Glu Arg Leu Ala Lys Asp Ile Met Lys Asp Ile	
44	45 50 55	
45	gga tat agt gac atc atg gtc ctg tgt gtg ctt aaa ggg ggg tac aaa	844
46	Gly Tyr Ser Asp Ile Met Val Leu Cys Val Leu Lys Gly Gly Tyr Lys	
47	60 65 70	
48	ttc tgt gct gat ctc gta gaa cac ctt aag aac atc agc cga aat tca	892
	Phe Cys Ala Asp Leu Val Glu His Leu Lys Asn Ile Ser Arg Asn Ser	

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49          75          80          85
50  gat cgg ttt gtc tca atg aag gtt gat ttc atc aga cta aaa agt tac      940
51  Asp Arg Phe Val Ser Met Lys Val Asp Phe Ile Arg Leu Lys Ser Tyr
52  90          95          100          105
53  agg aat gac cag tcc atg ggt gag atg cag ata atc gga ggc ggt gat      988
54  Arg Asn Asp Gln Ser Met Gly Glu Met Gln Ile Ile Gly Gly Gly Asp
55          110          115          120
56  ctt tca acg ctg gct gga aag aat ttt ctc att gtt gag gat gtt gtc      1036
57  Leu Ser Thr Leu Ala Gly Lys Asn Phe Leu Ile Val Glu Asp Val Val
58          125          130          135
59  gga act ggg agg acc atg aaa gca cta ctc agc aat ata gag aaa tac      1084
60  Gly Thr Gly Arg Thr Met Lys Ala Leu Leu Ser Asn Ile Glu Lys Tyr
61          140          145          150
62  aag ccc aac atg att aag gta gcc agt ttg ttg gtg aag aga aca tcc      1132
63  Lys Pro Asn Met Ile Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser
64          155          160          165
65  aga agt gac ggc ttt aga cct gac tat gct gga ttt gag att cca cac      1180
66  Arg Ser Asp Gly Phe Arg Pro Asp Tyr Ala Gly Phe Glu Ile Pro His
67          170          175          180          185
68  tta ttt gtg gtg gga tat gcc tta gat tac aat gaa tac ttc aga gat      1228
69  Leu Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp
70          190          195          200
71  ctg aat cac ata tgc gtc atc aat gag cac ggg taa aggaaaaatat      1274
72  Leu Asn His Ile Cys Val Ile Asn Glu His Gly
73          205          210
74  cgagtccttaa agacatgaat tctcaccact aaaggcccca gataggatca tttttacgcc      1334
75  tgtcttgggg agccagttgc aagttggggc cccccggatc ttcatcagga gg      1386
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 212
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
81 <400> SEQUENCE: 2
82  Met Ala Thr Arg Ser Pro Gly Val Val Ile Met Asp Asp Trp Pro Gly
83  1          5          10          15
84  Tyr Asp Leu Asn Leu Phe Thr Tyr Pro Gln His Tyr Tyr Gly Asp Leu
85          20          25          30
86  Glu Tyr Val Leu Ile Pro His Gly Ile Ile Val Asp Arg Ile Glu Arg
87          35          40          45
88  Leu Ala Lys Asp Ile Met Lys Asp Ile Gly Tyr Ser Asp Ile Met Val
89          50          55          60
90  Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Cys Ala Asp Leu Val Glu
91          65          70          75          80
92  His Leu Lys Asn Ile Ser Arg Asn Ser Asp Arg Phe Val Ser Met Lys
93          85          90          95
94  Val Asp Phe Ile Arg Leu Lys Ser Tyr Arg Asn Asp Gln Ser Met Gly
95          100          105          110
96  Glu Met Gln Ile Ile Gly Gly Gly Asp Leu Ser Thr Leu Ala Gly Lys
97          115          120          125
98  Asn Phe Leu Ile Val Glu Asp Val Val Gly Thr Gly Arg Thr Met Lys

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99          130          135          140
100      Ala Leu Leu Ser Asn Ile Glu Lys Tyr Lys Pro Asn Met Ile Lys Val
101          145          150          155          160
102      Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Asp Gly Phe Arg Pro
103          165          170          175
104      Asp Tyr Ala Gly Phe Glu Ile Pro His Leu Phe Val Val Gly Tyr Ala
105          180          185          190
106      Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile
107          195          200          205
108      Asn Glu His Gly
109          210
111 <210> SEQ ID NO: 3
112 <211> LENGTH: 37
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Primer for PCR
117 <400> SEQUENCE: 3
118      tccgttatgg cgacccgcag ccctggcgctc gtgatta
120 <210> SEQ ID NO: 4
121 <211> LENGTH: 21
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Primer for PCR
126 <400> SEQUENCE: 4
127      catcaatgag cacgggtaaa g
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 24
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Primer for PCR
135 <400> SEQUENCE: 5
136      gatcggagac tacgggcgaa tggc
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 27
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Primer for PCR
144 <400> SEQUENCE: 6
145      caggtgcatc aatgagcacg ggtaaag
147 <210> SEQ ID NO: 7
148 <211> LENGTH: 218
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
151 <400> SEQUENCE: 7
152      Met Ala Thr Arg Ser Pro Gly Val Val Ile Ser Asp Asp Glu Pro Gly

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153      1          5          10          15
154      Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Ala Glu Asp Leu
155              20          25          30
156      Glu Arg Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
157              35          40          45
158      Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
159              50          55          60
160      Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
161              65          70          75          80
162      Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
163              85          90          95
164      Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
165              100          105          110
166      Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
167              115          120          125
168      Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
169              130          135          140
170      Thr Leu Leu Ser Leu Val Arg Gln Tyr Asn Pro Lys Met Val Lys Val
171              145          150          155          160
172      Ala Ser Leu Leu Val Lys Arg Thr Pro Arg Ser Val Gly Tyr Lys Pro
173              165          170          175
174      Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
175              180          185          190
176      Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Val Cys Val Ile
177              195          200          205
178      Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
179              210          215
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 218
183 <212> TYPE: PRT
184 <213> ORGANISM: Cricetulus longicaudatus
185 <400> SEQUENCE: 8
186      Met Ala Thr Arg Ser Pro Ser Val Val Ile Ser Asp Asp Glu Pro Gly
187      1          5          10          15
188      Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Val Glu Asp Leu
189              20          25          30
190      Glu Lys Val Phe Ile Pro His Gly Val Ile Met Asp Arg Thr Glu Arg
191              35          40          45
192      Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
193              50          55          60
194      Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
195              65          70          75          80
196      Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
197              85          90          95
198      Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
199              100          105          110
200      Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
201              115          120          125
202      Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln

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203          130          135          140
204      Thr Leu Leu Ser Leu Val Lys Arg Tyr Asn Pro Lys Met Val Lys Val
205          145          150          155          160
206      Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
207          165          170          175
208      Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
209          180          185          190
210      Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile
211          195          200          205
212      Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
213          210          215
215 <210> SEQ ID NO: 9
216 <211> LENGTH: 231
217 <212> TYPE: PRT
218 <213> ORGANISM: Plasmodium falciparum
219 <400> SEQUENCE: 9
220      Met Pro Ile Pro Asn Asn Pro Gly Ala Gly Glu Asn Ala Phe Asp Pro
221          1          5          10          15
222      Val Phe Val Lys Asp Asp Asp Gly Tyr Asp Leu Asp Ser Phe Met Ile
223          20          25          30
224      Pro Ala His Tyr Lys Lys Tyr Leu Thr Lys Val Leu Val Pro Asn Gly
225          35          40          45
226      Val Ile Lys Asn Arg Ile Glu Lys Leu Ala Tyr Asp Ile Lys Lys Val
227          50          55          60
228      Tyr Asn Asn Glu Glu Phe His Ile Leu Cys Leu Leu Lys Gly Ser Arg
229          65          70          75          80
230      Gly Phe Phe Thr Ala Leu Leu Lys His Leu Ser Arg Ile His Asn Tyr
231          85          90          95
232      Ser Ala Val Glu Met Ser Lys Pro Leu Phe Gly Glu His Tyr Val Arg
233          100          105          110
234      Val Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly Thr Leu Glu Ile Val
235          115          120          125
236      Ser Glu Asp Leu Ser Cys Leu Lys Gly Lys His Val Leu Ile Val Glu
237          130          135          140
238      Asp Ile Ile Asp Thr Gly Lys Thr Leu Val Lys Phe Cys Glu Tyr Leu
239          145          150          155          160
240      Lys Lys Phe Glu Ile Lys Thr Val Ala Ile Ala Cys Leu Phe Ile Lys
241          165          170          175
242      Arg Thr Pro Leu Trp Asn Gly Phe Lys Ala Asp Phe Val Gly Phe Ser
243          180          185          190
244      Ile Pro Asp His Phe Val Val Gly Tyr Ser Leu Asp Tyr Asn Glu Ile
245          195          200          205
246      Phe Arg Asp Leu Asp His Cys Cys Leu Val Asn Asp Glu Gly Lys Lys
247          210          215          220
248      Lys Tyr Lys Ala Thr Ser Leu
249          225          230
251 <210> SEQ ID NO: 10
252 <211> LENGTH: 210
253 <212> TYPE: PRT

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VERIFICATION SUMMARY

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